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RAW SEQUENCE LISTING

DATE: 02/06/2002

PATENT APPLICATION: US/10/014,156

TIME: 09:40:49

Input Set : N:\Crf3\RULE60\10014156.raw

Output Set: N:\CRF3\02062002\J014156.raw

ENTERED

1 <110> APPLICANT: Hilton, Douglas J.
 2 Willson, Tracy
 3 Nicola, Nicos A.
 4 Gainsford, Timothy
 5 Alexander, Warren S.
 6 Metcalf, Donald
 7 Ng, Ashley
 8 <120> TITLE OF INVENTION: A NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES
 9 ENCODING SAME
 10 <130> FILE REFERENCE: 11268
 12 <140> CURRENT APPLICATION NUMBER: 10/014,156
 13 <141> CURRENT FILING DATE: 2001-12-07
 15 <150> PRIOR APPLICATION NUMBER: US/09/043,816
 16 <151> PRIOR FILING DATE: 1998-09-17
 19 <160> NUMBER OF SEQ ID NOS: 44
 20 <170> SOFTWARE: PatentIn Ver. 2.0
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 25 <213> ORGANISM: Artificial Sequence
 26 <220> FEATURE:
 27 <223> OTHER INFORMATION: Description of Artificial Sequence:Synthetic
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 35 <220> FEATURE:
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 37 <400> SEQUENCE: 2
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 41 <211> LENGTH: 19
 42 <212> TYPE: DNA
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 50 <211> LENGTH: 21
 51 <212> TYPE: DNA

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52 <213> ORGANISM: Artificial Sequence
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65     ctcagctaca tccctgctag t                                21
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76 <210> SEQ ID NO: 7
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89 <220> FEATURE:
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104 <211> LENGTH: 34
105 <212> TYPE: DNA
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107 <220> FEATURE:
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127 <222> LOCATION: (27)..(68)
128 <223> OTHER INFORMATION: N is a or g or c or t
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130 <222> LOCATION: (923)
131 <223> OTHER INFORMATION: R is g or a
132 <221> NAME/KEY: unsure
133 <222> LOCATION: (2315)
134 <223> OTHER INFORMATION: S is g or c
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138      ttagaggatt atggatttgg cagttcaccc tgaccatctt gaaaataagt tatctctgat 180
139      ctctgtctgt atgttacttc tctccctcca ccaacggaga acaaagtggg gcaaagtgtg 240
140      cttctctgaa gtaagatgat ttgtcaaaaa ttctgtgtgg ttttgttaca ttgggaattt 300
141      atttatgtga taactgcgtt taacttgtca tatccaatta ctcttgagg attttaagttg 360
142      tcttgcatgc caccaaattc aacctatgac tacttccctt tgctgtctgg actctcaaag 420
143      aataacttcaa attcgaatgg acattatgag acagctgttg aacctaaagt taattcaagt 480
144      ggtactcact tttctaactt atccaaaaca actttccact gttgctttcg gagtgcagca 540
145      gatagaaact gctccttatg tgcagacaac attgaaggaa ggacatttgt ttcaacagta 600
146      aattcttttag tttttcaaca aatagatgca aactggaaca tacagtgcgt gctaaaagga 660
147      gacttaaaat tattcatctg ttatgtggag tcattattta agaatctatt caggaattat 720
148      aactataagg tccatctttt atatgttctg cctgaagtgt tagaagattc acctctggtt 780
149      ccccaaaaag gcagttttca gatggttcac tgcaattgca gtgttcatga atgttgatga 840
150      tgtcttgtgc ctgtgccaac agccaaactc aacgacactc tccttatgtg tttgaaaatc 900
151      acatctgggtg gagtaatttt ccrgtcacct ctaatgtcag ttcagcccat aaatatgggtg 960
152      aagcctgac caccattagg tttgcatatg gaaatcacag atgatggtaa tttaaagatt 1020
153      tcttggtcca gccaccattt ggtaccattt ccacttcaat atcaagtga atattcagag 1080
154      aattctacaa cagttatcag agaagctgac aagattgtct cagctacatc cctgctagta 1140
155      gacagtatac ttcctgggtc ttcgtatgag gttcagggtg ggggcaagag actggatggc 1200
156      ccaggaatct ggagtgactg gagtactcct cgtgtcttta ccacacaaga tgtcatatac 1260
157      tttccaccta aaattctgac aagtgttggg tctaattgtt cttttcactg catctataag 1320

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158      aaggaaaaca agattgttcc ctcaaaagag attgtttggt ggatgaattt agctgagaaa 1380
159      attcctcaaa gccagtatga tgttgtgagt gatcatgtta gcaaagttag ttttttcaat 1440
160      ctgaatgaaa ccaaacctcg aggaaagttt acctatgatg cagtgtactg ctgcaatgaa 1500
161      catgaatgcc atcatcgcta tgctgaatta tatgtgattg atgtcaatat caatatctca 1560
162      tgtgaaactg atgggtactt aactaaaatg acttgcagat ggtcaaccag tacaatccag 1620
163      tcacttgcgg aaagcacttt gcaattgagg tatcatagga gcagccttta ctgttctgat 1680
164      attccatcta ttcattccat atctgagccc aaagattgct atttgcagag tgatggtttt 1740
165      tatgaatgca ttttccagcc aatcttccta ttatctggct acacaatgtg gattaggatc 1800
166      aatcactctc taggttcact tgactctcca ccaacatgtg tccttctga ttctgtggtg 1860
167      aagccactgc ctccatccag tgtgaaagca gaaattacta taaacattgg attattgaaa 1920
168      atatcttggg aaaagccagt ctttccagag aataaccttc aattccagat tcgctatggt 1980
169      ttaagtggaa aagaagtaca atggaagatg tatgaggttt atgatccaaa accaaaatct 2040
170      gtcagtctcc cagttccaga cttgtgtgca gtctatgctg ttcagggtggc gtttaagagg 2100
171      ctagatggac tgggatattg gagtaattgg agcaatccag cctacacagt tgtcatggat 2160
172      ataaaagttc ctatgagagg acctgaattt tggagaataa ttaatggaga tactatgaaa 2220
173      aaggagaaaa atgtcacttt actttggaag cccctgatga aaaatgactc attgtgcagt 2280
174      gttcagagat atgtgataaa ccatcatact tcctscatg gaacatggtc agaagatgtg 2340
175      ggaaatcaca cgaaattcac tttcctgtgg acagagcaag cacatactgt tacggttctg 2400
176      gccatcaatt caattggtgc ttctgttgca aattttaatt taaccttttc atggcctatg 2460
177      agcaaagtaa atatcgtgca gtcactcagt gcttatcctt taaacagcag ttgtgtgatt 2520
178      gtttcctgga tactatcacc cagtgttacc aagctaattg attttattat tgatggaaa 2580
179      aatcttaatg aagatggtga aataaaatgg cttagaatct cttcatctgt taagaagtat 2640
180      tatatccatg atcatcttat cccattgag aagtaccagt tcagtcttta cccaatattt 2700
181      atggaaggag tgggaaaacc aaagataatt aatagtttca ctcaagatga tattgaaaaa 2760
182      caccagagtg atgcaggttt atatgtaatt gtgccagtaa ttatttcctc ttccatctta 2820
183      ttgcttgga cattaatta atcacaccaa agaatgaaaa agctattttg ggaagatgtt 2880
184      ccgaaccca agaattgttc ctgggcacaa ggacttaatt ttcagaagag aacggacatt 2940
185      ctttgaagtc taatcatgat cactacagat gaaccaatg tgccaacttc ccaacagctc 3000
186      atagagtatt agaagatttt tacattttga agaaggggag caaatctaaa aaaaattcag 3060
187      ttgaacttct gagagttaac atatggtgga ttatgttgat ttagaactta aaatagatgt 3120
188      catttaaacc caagttttac atctaaactc aggtcaaacc tacacactaa ttaaaagttt 3180
189      agtagatttc aaattttcat cafaagtact aaagaccgaa aactaaacag tataaggacc 3240
190      agtattttgt aattctttta ataccgacaa cgacagtaat gtatagataa ttacagtag 3300
191      tttatacatc atctgttagg acattaatcc acttgagatt ttgacgttgt agactgttta 3360
192      tcgaaatttt tatgttacta atattcatac cttagtcact tttataaatc aaacataaaa 3420
193      atacagttt gaaaaggtaa aatctaagga aatatctgtg cagtcggatt tttagtcgga 3480
194      taagcccaca agaaaactta tagaggaccg taaaaacata gattgaaaca agttagacc 3540
195      ttaaaagcaa aggttatagg aacttttacc gaattcacta ttgaaggcaa agtcaatttt 3600
196      ccttcgggct tcaacacaaa cagcagcggg gtctgtgcac cctcaatgtc aagtatagtc 3660
197      ctactgggat gtatgggtcc agtctaactg ccctgggtct ccctgttagc tgaagattac 3720
198      aggtgcgaaa gaacaaatta atactggatt tagattaaat gaagtgact tggtaggttc 3780
199      tggagaccgt ccgtcccttt acccgtaact asgttttttc cctctgagaa acctcgaaa 3840
200      tacttatcaa gtaccactcc tgtcttgaag agatgaaagt ctgtctgacg aacgatcaaa 3900
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203 <210> SEQ ID NO: 13
204 <211> LENGTH: 896
205 <212> TYPE: PRT
206 <213> ORGANISM: Homo sapiens
207 <220> FEATURE:

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210 <223> OTHER INFORMATION: Xaa is unknown or other.
211 <221> NAME/KEY: UNSURE
212 <222> LOCATION: (687)
213 <223> OTHER INFORMATION: Xaa is unknown or other.
214 <400> SEQUENCE: 13
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216       1           5           10           15
217   Tyr Val Ile Thr Ala Phe Asn Leu Ser Tyr Pro Ile Thr Pro Trp Arg
218       20           25           30
219   Phe Lys Leu Ser Cys Met Pro Pro Asn Ser Thr Thr Asn Tyr Phe Leu
220       35           40           45
221   Leu Pro Ala Gly Leu Ser Lys Asn Thr Ser Asn Ser Asn Gly His Tyr
222       50           55           60
223   Glu Thr Ala Val Glu Pro Lys Phe Asn Ser Ser Gly Thr His Phe Ser
224       65           70           75           80
225   Asn Leu Ser Lys Thr Thr Phe His Cys Cys Phe Arg Ser Glu Gln Asp
226       85           90           95
227   Arg Asn Cys Ser Leu Cys Ala Asp Asn Ile Glu Gly Arg Thr Phe Val
228       100          105          110
229   Ser Thr Val Asn Ser Leu Val Phe Gln Gln Ile Asp Ala Asn Trp Asn
230       115          120          125
231   Ile Gln Cys Trp Leu Lys Gly Asp Leu Lys Leu Phe Ile Cys Tyr Val
232       130          135          140
233   Glu Ser Leu Phe Lys Asn Leu Phe Arg Asn Tyr Asn Tyr Lys Val His
234       145          150          155          160
235   Leu Leu Tyr Val Leu Pro Glu Val Leu Glu Asp Ser Pro Leu Val Pro
236       165          170          175
237   Gln Lys Gly Ser Phe Gln Met Val His Cys Asn Cys Ser Val His Glu
238       180          185          190
239   Cys Cys Glu Cys Leu Val Pro Val Pro Thr Ala Lys Leu Asn Asp Thr
240       195          200          205
W--> 241   Leu Leu Met Cys Leu Lys Ile Thr Ser Gly Gly Val Ile Phe Xaa Ser
242       210          215          220
243   Pro Leu Met Ser Val Gln Pro Ile Asn Met Val Lys Pro Asp Pro Pro
244       225          230          235          240
245   Leu Gly Leu His Met Glu Ile Thr Asp Asp Gly Asn Leu Lys Ile Ser
246       245          250          255
247   Trp Ser Ser Pro Pro Leu Val Pro Phe Pro Leu Gln Tyr Gln Val Lys
248       260          265          270
249   Tyr Ser Glu Asn Ser Thr Thr Val Ile Arg Glu Ala Asp Lys Ile Val
250       275          280          285
251   Ser Ala Thr Ser Leu Leu Val Asp Ser Ile Leu Pro Gly Ser Ser Tyr
252       290          295          300
253   Glu Val Gln Val Arg Gly Lys Arg Leu Asp Gly Pro Gly Ile Trp Ser
254       305          310          315          320
255   Asp Trp Ser Thr Pro Arg Val Phe Thr Thr Gln Asp Val Ile Tyr Phe
256       325          330          335

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VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\10014156.raw

Output Set: N:\CRF3\02062002\J014156.raw

L:136 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:137 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:241 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:299 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:441 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:619 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44